

Seq. No. 163405
 Seq. ID LIB3177-062-P1-K1-F1
 Method BLASTX
 NCBI GI g2252828
 BLAST score 455
 E value 2.0e-45
 Match length 121
 % identity 80
 NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 163406
 Seq. ID LIB3177-062-P1-K1-F10
 Method BLASTX
 NCBI GI g3128217
 BLAST score 473
 E value 2.0e-47
 Match length 110
 % identity 87
 NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
 >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 163407
 Seq. ID LIB3177-062-P1-K1-F11
 Method BLASTX
 NCBI GI g1773014
 BLAST score 300
 E value 2.0e-27
 Match length 89
 % identity 70
 NCBI Description (Y10338) chloride channel Stclcl [Solanum tuberosum]

Seq. No. 163408
 Seq. ID LIB3177-062-P1-K1-F12
 Method BLASTX
 NCBI GI g2062161
 BLAST score 678
 E value 2.0e-71
 Match length 140
 % identity 50
 NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No. 163409
 Seq. ID LIB3177-062-P1-K1-F2
 Method BLASTX
 NCBI GI g3885511
 BLAST score 366
 E value 4.0e-35
 Match length 95
 % identity 79
 NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No. 163410
 Seq. ID LIB3177-062-P1-K1-F4

Method BLASTX
 NCBI GI g4741960
 BLAST score 574
 E value 2.0e-59
 Match length 128
 % identity 85
 NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 163411
 Seq. ID LIB3177-062-P1-K1-F5
 Method BLASTN
 NCBI GI g4249393
 BLAST score 103
 E value 6.0e-51
 Match length 131
 % identity 95
 NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163412
 Seq. ID LIB3177-062-P1-K1-F6
 Method BLASTX
 NCBI GI g2104957
 BLAST score 584
 E value 2.0e-60
 Match length 107
 % identity 100
 NCBI Description (U96924) immunophilin [Arabidopsis thaliana]

Seq. No. 163413
 Seq. ID LIB3177-062-P1-K1-F7
 Method BLASTX
 NCBI GI g3413714
 BLAST score 364
 E value 7.0e-35
 Match length 105
 % identity 22
 NCBI Description (AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No. 163414
 Seq. ID LIB3177-062-P1-K1-F8
 Method BLASTN
 NCBI GI g3985958
 BLAST score 286
 E value 1.0e-160
 Match length 419
 % identity 99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 163415
 Seq. ID LIB3177-062-P1-K1-F9
 Method BLASTN
 NCBI GI g2760167
 BLAST score 127
 E value 3.0e-65

Seq. ID	LIB3177-062-P1-K1-G9
Method	BLASTX
NCBI GI	g3096931
BLAST score	576
E value	1.0e-59
Match length	113
% identity	99
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	163427
Seq. ID	LIB3177-062-P1-K1-H10
Method	BLASTN
NCBI GI	g2281081
BLAST score	227
E value	1.0e-125
Match length	227
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163428
Seq. ID	LIB3177-062-P1-K1-H11
Method	BLASTN
NCBI GI	g2351062
BLAST score	210
E value	1.0e-114
Match length	362
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163429
Seq. ID      LIB3177-062-P1-K1-H2
Method       BLASTX
NCBI GI      g2199574
BLAST score   340
E value      2.0e-32
Match length  65
% identity    98
NCBI Description (AF004293) aquaporin [Brassica rapa]
```

```
Seq. No.      163430
Seq. ID      LIB3177-062-P1-K1-H3
Method       BLASTX
NCBI GI      g3914658
BLAST score   294
E value      5.0e-27
Match length  74
% identity    80
NCBI Description  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
                >gi_1694974_emb_CAA70851_(Y09635) plastid ribosomal
                protein [Arabidopsis thaliana]
```

```
Seq. No.      163431
Seq. ID      LIB3177-062-P1-K1-H4
Method       BLASTX
```

```

NCBI GI          g2506443
BLAST score      553
E value          6.0e-57
Match length     139
% identity       78
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_2117520_pir_JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]

```

```
Seq. No.      163432
Seq. ID      LIB3177-062-P1-K1-H5
Method       BLASTX
NCBI GI      g113026
BLAST score   372
E value      9.0e-63
Match length  135
% identity    87
NCBI Description  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
>gi_68211_pir_WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
isocitrate lyase [Brassica napus]
```

```
Seq. No.      163433
Seq. ID       LIB3177-062-P1-K1-H6
Method        BLASTX
NCBI GI       g4741952
BLAST score   98
E value       8.0e-66
Match length  125
% identity    60
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
```

```
Seq. No.      163434
Seq. ID      LIB3177-062-P1-K1-H7
Method       BLASTX
NCBI GI      g132090
BLAST score   618
E value      2.0e-64
Match length  113
% identity    99
NCBI Description  RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir_RKMUB1
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700-
                (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                thaliana]
```

Seq. No. 163435

Seq. ID LIB3177-062-P1-K1-H9
 Method BLASTN
 NCBI GI g4587641
 BLAST score 165
 E value 1.0e-87
 Match length 286
 % identity 99
 NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No. 163436
 Seq. ID LIB3177-063-P1-K1-A12
 Method BLASTN
 NCBI GI g3047100
 BLAST score 90
 E value 2.0e-43
 Match length 122
 % identity 94
 NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 163437
 Seq. ID LIB3177-063-P1-K1-A3
 Method BLASTN
 NCBI GI g4756963
 BLAST score 280
 E value 1.0e-156
 Match length 326
 % identity 95
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No. 163438
 Seq. ID LIB3177-063-P1-K1-A4
 Method BLASTX
 NCBI GI g2661422
 BLAST score 442
 E value 3.0e-57
 Match length 122
 % identity 94
 NCBI Description (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No. 163439
 Seq. ID LIB3177-063-P1-K1-A5
 Method BLASTX
 NCBI GI g3157947
 BLAST score 361
 E value 7.0e-35
 Match length 74
 % identity 53
 NCBI Description (AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

```
Seq. No.      163440
Seq. ID      LIB3177-063-P1-K1-A6
Method       BLASTX
NCBI GI      g3892722
BLAST score   534
E value      1.0e-54
Match length  120
% identity    92
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      163441
Seq. ID      LIB3177-063-P1-K1-A7
Method       BLASTX
NCBI GI      g121075
BLAST score   259
E value      5.0e-23
Match length  63
% identity    84
NCBI Description  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725
(M82921) H-Protein precursor [Arabidopsis thaliana]
>gi_861215 (U27144) glycine decarboxylase complex H-protein
precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
glycine decarboxylase complex H-protein [Arabidopsis
thaliana] >gi_445119_prf_1908425A Gly
decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
```

```
Seq. No.      163442
Seq. ID      LIB3177-063-P1-K1-B1
Method       BLASTX
NCBI GI      g115385
BLAST score   216
E value      5.0e-18
Match length  43
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
```

```
Seq. No.      163443
Seq. ID      LIB3177-063-P1-K1-B11
Method       BLASTN
NCBI GI      g4455262
BLAST score   97
E value      2.0e-47
Match length  217
% identity    58
NCBI Description  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                (ESSAII project)
```

```
Seq. No.      163444
Seq. ID      LIB3177-063-P1-K1-B12
Method       BLASTX
NCBI GI      g4587564
BLAST score   364
E value      1.0e-72
Match length  145
```


% identity	68
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence
Seq. No.	163455
Seq. ID	LIB3177-063-P1-K1-C5
Method	BLASTN
NCBI GI	g4733953
BLAST score	138
E value	1.0e-71
Match length	285
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F13011 genomic sequence, complete sequence
Seq. No.	163456
Seq. ID	LIB3177-063-P1-K1-C6
Method	BLASTX
NCBI GI	g1488604
BLAST score	147
E value	2.0e-09
Match length	36
% identity	86
NCBI Description	(Z49842) ribulosebiphosphate carboxylase [Hordeum lechleri]
Seq. No.	163457
Seq. ID	LIB3177-063-P1-K1-C7
Method	BLASTN
NCBI GI	g4757405
BLAST score	154
E value	3.0e-81
Match length	347
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence
Seq. No.	163458
Seq. ID	LIB3177-063-P1-K1-C8
Method	BLASTN
NCBI GI	g3046849
BLAST score	209
E value	1.0e-114
Match length	213
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.	163459
Seq. ID	LIB3177-063-P1-K1-C9
Method	BLASTX
NCBI GI	g1170939
BLAST score	687
E value	1.0e-72
Match length	139
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163479
Seq. ID      LIB3177-063-P1-K1-F12
Method       BLASTX
NCBI GI      g548355
BLAST score   459
E value      4.0e-46
Match length  100
% identity    91
NCBI Description  NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate
reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
>gi_22757_emb_CAA79494_(Z19050) nitrate reductase
[Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate
reductase [Arabidopsis thaliana]
```

```
Seq. No.      263480
Seq. ID      LIB3177-063-P1-K1-F2
Method       BLASTX
NCBI GI      g136636
BLAST score   288
E value      9.0e-26
Match length  75
% identity    80
NCBI Description  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 -
                Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin
                Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                [Arabidopsis thaliana]
```

```
Seq. No.      163481
Seq. ID      LIB3177-063-P1-K1-F3
Method       BLASTX
NCBI GI      g1363489
BLAST score   691
E value      4.0e-73
Match length  128
% identity    99
NCBI Description  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
glucohydrolase [Arabidopsis thaliana]
```

Seq. No.	163482
Seq. ID	LIB3177-063-P1-K1-F4
Method	BLASTX
NCBI GI	g4678260
BLAST score	497
E value	3.0e-50
Match length	121
% identity	86
NCBI Description	(AL049657) putative protein [Arabidopsis thaliana]

Seq. No. 163483


```

NCBI GI      g4454048
BLAST score   61
E value      4.0e-70
Match length 131
% identity   99
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

```

```
Seq. No.      163489
Seq. ID       LIB3177-063-P1-K1-G3
Method        BLASTX
NCBI GI       g115767
BLAST score    531
E value       7.0e-65
Match length   129
% identity     98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR  
                (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll  
                a/b-binding protein ab165 - Arabidopsis thaliana  
                >gi_16368_emb_CAA27540_(X03907) chlorophyll a/b binding  
                protein [LHCF AB 65] [Arabidopsis thaliana]  
                >gi_16372_emb_CAA27541_(X03908) chlorophyll a/b binding  
                protein (LHCF AB 180) [Arabidopsis thaliana]
```

```
Seq. No.      163490
Seq. ID      LIB3177-063-P1-K1-G4
Method       BLASTX
NCBI GI      g1076308
BLAST score   428
E value      3.0e-42
Match length  123
% identity    72
NCBI Description RNA-binding protein cp33 precursor - Arabidopsis thaliana
               >gi_681910_dbj_BAA06522_ (D31714) cp33 [Arabidopsis
               thaliana]
```

```
Seq. No.      163491
Seq. ID       LIB3177-063-P1-K1-G6
Method        BLASTX
NCBI GI       g4204266
BLAST score   323
E value       1.0e-53
Match length  128
% identity    93
NCBI Description (AC005223) 52263 [Arabidopsis thaliana]
```

```

Seq. No.      163492
Seq. ID       LIB3177-063-P1-K1-G8
Method        BLASTX
NCBI GI       g132074
BLAST score   602
E value       9.0e-63
Match length  110
% identity    100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir_RKMUA1
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                A1 precursor - Arabidopsis thaliana

```



```
Method          BLASTX
NCBI GI         g541858
BLAST score     614
E value        8.0e-64
Match length    127
% identity      98
NCBI Description endoxyloglucan transferase - Arabidopsis thaliana
                 >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
                 transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                 endo-xyloglucan transferase [Arabidopsis thaliana]
```

```
Seq. No.      163523
Seq. ID      LIB3177-064-P1-K1-C3
Method       BLASTX
NCBI GI      g136636
BLAST score   469
E value      5.0e-47
Match length  87
% identity    99
NCBI Description  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 -
                Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin
                Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                [Arabidopsis thaliana]
```

```
Seq. No.      163524
Seq. ID       LIB3177-064-P1-K1-C5
Method        BLASTX
NCBI GI       g2956690
BLAST score   433
E value       6.0e-43
Match length  116
% identity    58
NCBI Description (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928
                 (AF079800) PsbY precursor [Arabidopsis thaliana]
```

```
Seq. No.      163525
Seq. ID      LIB3177-064-P1-K1-C6
Method       BLASTX
NCBI GI      g2506443
BLAST score   279
E value      4.0e-25
Match length  87
% identity    69
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_2117520_pir_JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]
```



```
Method          BLASTX
NCBI GI         g2499609
BLAST score     280
E value         3.0e-25
Match length    53
% identity      100
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5)
                 (ATMPK5) >gi_629546_pir_S40471 mitogen-activated protein
                 kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana
                 >gi_457402_dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis
                 thaliana]
```

```
Seq. No.      163537
Seq. ID      LIB3177-064-P1-K1-D7
Method       BLASTX
NCBI GI      g4218120
BLAST score   461
E value      4.0e-46
Match length  116
% identity    78
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis
thaliana]
```

```
Seq. No.      163538
Seq. ID       LIB3177-064-P1-K1-D8
Method        BLASTX
NCBI GI       g3212869
BLAST score   809
E value       7.0e-87
Match length  153
% identity    99
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
```

Seq. No.	163539
Seq. ID	LIB3177-064-P1-K1-D9
Method	BLASTN
NCBI GI	g4584351
BLAST score	284
E value	1.0e-159
Match length	336
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

```

Seq. No.          163540
Seq. ID           LIB3177-064-P1-K1-E10
Method            BLASTX
NCBI GI           g132166
BLAST score       161
E value           3.0e-11
Match length      56
% identity        66
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir_S04048
                  ribulose-bisphosphate carboxylase activase precursor -
                  Arabidopsis thaliana >gi_16471_emb_CAA32429 (X14212)
                  rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

```


BLAST score 173
 E value 2.0e-92
 Match length 392
 % identity 96
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No. 163550
 Seq. ID LIB3177-064-P1-K1-F12
 Method BLASTX
 NCBI GI g2143227
 BLAST score 167
 E value 3.0e-12
 Match length 46
 % identity 74
 NCBI Description (Y13356) glyoxysomal isocitrate lyase [Brassica napus]

Seq. No. 163551
 Seq. ID LIB3177-064-P1-K1-F2
 Method BLASTN
 NCBI GI g4468801
 BLAST score 141
 E value 1.0e-73
 Match length 212
 % identity 98
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No. 163552
 Seq. ID LIB3177-064-P1-K1-F4
 Method BLASTX
 NCBI GI g4467099
 BLAST score 389
 E value 5.0e-38
 Match length 75
 % identity 100
 NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No. 163553
 Seq. ID LIB3177-064-P1-K1-F5
 Method BLASTN
 NCBI GI g3449334
 BLAST score 117
 E value 3.0e-59
 Match length 230
 % identity 98
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No. 163554
 Seq. ID LIB3177-064-P1-K1-F7
 Method BLASTX
 NCBI GI g3286693
 BLAST score 632
 E value 3.0e-66
 Match length 127

BLAST score 164
 E value 2.0e-23
 Match length 74
 % identity 71
 NCBI Description (X61664) photosystem I psaH protein [Nicotiana sylvestris]

Seq. No. 163570
 Seq. ID LIB3177-064-P1-K1-H4
 Method BLASTX
 NCBI GI g4741948
 BLAST score 755
 E value 2.0e-80
 Match length 142
 % identity 100
 NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 163571
 Seq. ID LIB3177-064-P1-K1-H5
 Method BLASTX
 NCBI GI g115470
 BLAST score 308
 E value 3.0e-28
 Match length 133
 % identity 51
 NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir_S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana
 >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No. 163572
 Seq. ID LIB3177-064-P1-K1-H7
 Method BLASTX
 NCBI GI g1769905
 BLAST score 303
 E value 9.0e-28
 Match length 99
 % identity 62
 NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving complex (OEC) [Arabidopsis thaliana]

Seq. No. 163573
 Seq. ID LIB3177-064-P1-K1-H8
 Method BLASTX
 NCBI GI g4587527
 BLAST score 167
 E value 3.0e-12
 Match length 66
 % identity 56
 NCBI Description (AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No. 163574
 Seq. ID LIB3177-064-P1-K1-H9
 Method BLASTX
 NCBI GI g4204285

Seq. ID LIB3177-065-P1-K1-A2
 Method BLASTX
 NCBI GI g3395441
 BLAST score 219
 E value 9.0e-18
 Match length 62
 % identity 58
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 163580
 Seq. ID LIB3177-065-P1-K1-A4
 Method BLASTX
 NCBI GI g1363489
 BLAST score 751
 E value 4.0e-80
 Match length 143
 % identity 95
 NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_(X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 163581
 Seq. ID LIB3177-065-P1-K1-A6
 Method BLASTX
 NCBI GI g2894596
 BLAST score 468
 E value 6.0e-47
 Match length 107
 % identity 85
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 163582
 Seq. ID LIB3177-065-P1-K1-A7
 Method BLASTX
 NCBI GI g2342684
 BLAST score 497
 E value 2.0e-50
 Match length 123
 % identity 84
 NCBI Description (AC000106) F7G19.14 [Arabidopsis thaliana]

Seq. No. 163583
 Seq. ID LIB3177-065-P1-K1-A8
 Method BLASTX
 NCBI GI g135467
 BLAST score 296
 E value 6.0e-27
 Match length 69
 % identity 100
 NCBI Description TUBULIN BETA-4 CHAIN >gi_2129546_pir_S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No. 163584
 Seq. ID LIB3177-065-P1-K1-A9
 Method BLASTX
 NCBI GI g1703446

```
BLAST score      194
E value          2.0e-15
Match length     54
% identity       76
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
>gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
thaliana]
```

```
Seq. No.      163585
Seq. ID       LIB3177-065-P1-K1-B1
Method        BLASTX
NCBI GI       g115783
BLAST score   557
E value       2.0e-57
Match length  107
% identity    98
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

Seq. No.	163586
Seq. ID	LIB3177-065-P1-K1-B10
Method	BLASTN
NCBI GI	g2737904
BLAST score	67
E value	1.0e-29
Match length	79
% identity	96
NCBI Description	Arabidopsis thaliana retrotransposon TSCL mRNA sequence

Seq. No.	163587
Seq. ID	LIB3177-065-P1-K1-B12
Method	BLASTN
NCBI GI	g2245031
BLAST score	298
E value	1.0e-167
Match length	318
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	163588
Seq. ID	LIB3177-065-P1-K1-B2
Method	BLASTN
NCBI GI	g2191126
BLAST score	318
E value	1.0e-179
Match length	334
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002N01

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Seq. No.      163589
Seq. ID      LIB3177-065-P1-K1-B3
Method       BLASTX
NCBI GI      q2119848
```



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NCBI GI      g4220457
BLAST score  493
E value      5.0e-50
Match length 112
% identity   38
NCBI Description (AC006216) Similar to gi_3413714 T19L18.21 putative
myrosinase-binding protein from Arabidopsis thaliana BAC
gb_AC004747. EST gb_N96478 comes from this gene.
[Arabidopsis thaliana]

```

```
Seq. No.      163594
Seq. ID      LIB3177-065-P1-K1-C1
Method       BLASTX
NCBI GI      g140508
BLAST score   308
E value      8.0e-29
Match length  65
% identity    88
NCBI Description  PROBABLE INTRON MATURASE >gi_99852_pir__S07168 probable
maturase, 63K - white mustard chloroplast
>gi_12220_emb_CAA28509_ (X04826) ycf14 (AA1-324) [Sinapis
alba]
```

Seq. No.	163595
Seq. ID	LIB3177-065-P1-K1-C10
Method	BLASTN
NCBI GI	g4741961
BLAST score	216
E value	1.0e-118
Match length	238
% identity	98
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

```
Seq. No.      163596
Seq. ID      LIB3177-065-P1-K1-C11
Method       BLASTX
NCBI GI      g1488255
BLAST score   346
E value      1.0e-32
Match length  90
% identity    69
NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
>gi_2961381_emb_CAA18128_(AL022141) ferulate-5-hydroxylase
[FAH1] [Arabidopsis thaliana] >gi_3925365 (AF068574)
ferulate-5-hydroxylase [Arabidopsis thaliana]
```

Seq. No.	163597
Seq. ID	LIB3177-065-P1-K1-C12
Method	BLASTN
NCBI GI	g4662609
BLAST score	76
E value	5.0e-35
Match length	159
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Match length	62
% identity	77
NCBI Description	(X85181) alpha-glucan phosphorylase [<i>Spinacia oleracea</i>]
Seq. No.	163603
Seq. ID	LIB3177-065-P1-K1-D1
Method	BLASTX
NCBI GI	g3355472
BLAST score	152
E value	2.0e-10
Match length	41
% identity	66
NCBI Description	(AC004218) disease resistance response protein (206-d) like [<i>Arabidopsis thaliana</i>]
Seq. No.	163604
Seq. ID	LIB3177-065-P1-K1-D10
Method	BLASTX
NCBI GI	g4220514
BLAST score	83
E value	4.0e-09
Match length	54
% identity	61
NCBI Description	(AL035356) putative protein [<i>Arabidopsis thaliana</i>]
Seq. No.	163605
Seq. ID	LIB3177-065-P1-K1-D11
Method	BLASTX
NCBI GI	g3236248
BLAST score	304
E value	6.0e-28
Match length	88
% identity	70
NCBI Description	(AC004684) unknown protein [<i>Arabidopsis thaliana</i>]
Seq. No.	163606
Seq. ID	LIB3177-065-P1-K1-D2
Method	BLASTX
NCBI GI	g1703220
BLAST score	441
E value	1.0e-43
Match length	141
% identity	57
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [<i>Arabidopsis thaliana</i>]
Seq. No.	163607
Seq. ID	LIB3177-065-P1-K1-D4
Method	BLASTX
NCBI GI	g227070
BLAST score	165
E value	1.0e-11
Match length	42
% identity	71
NCBI Description	ribosomal protein CS-S5 [<i>Spinacia oleracea</i>]
Seq. No.	163608

Seq. No.	163623
Seq. ID	LIB3177-065-P1-K1-F1
Method	BLASTN
NCBI GI	g3687221
BLAST score	58
E value	2.0e-24
Match length	86
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163624
Seq. ID	LIB3177-065-P1-K1-F10
Method	BLASTN
NCBI GI	g4589444
BLAST score	58
E value	3.0e-24
Match length	140
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence
Seq. No.	163625
Seq. ID	LIB3177-065-P1-K1-F4
Method	BLASTX
NCBI GI	g4006879
BLAST score	581
E value	2.0e-60
Match length	113
% identity	100
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.	163626
Seq. ID	LIB3177-065-P1-K1-F5
Method	BLASTX
NCBI GI	g3953473
BLAST score	452
E value	4.0e-45
Match length	117
% identity	80
NCBI Description	(AC002328) F2202.18 [Arabidopsis thaliana]
Seq. No.	163627
Seq. ID	LIB3177-065-P1-K1-F7
Method	BLASTN
NCBI GI	g4589428
BLAST score	265
E value	1.0e-147
Match length	289
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence
Seq. No.	163628
Seq. ID	LIB3177-065-P1-K1-F8
Method	BLASTX
NCBI GI	g4567235


```
Seq. ID      LIB3177-065-P1-K1-H12
Method       BLASTX
NCBI GI      g2244881
BLAST score   512
E value      4.0e-52
Match length  103
% identity    61
NCBI Description (Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]
```

```
Seq. No.      163644
Seq. ID      LIB3177-065-P1-K1-H3
Method       BLASTX
NCBI GI      g2559012
BLAST score   361
E value      1.0e-34
Match length  92
% identity    76
NCBI Description (AF026293) chaperonin containing t-complex polypeptide 1,
beta subunit; CCT-beta [Homo sapiens] >gi_4090929
(AF026166) chaperonin-containing TCP-1 beta subunit homolog
[Homo sapiens]
```

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Seq. No.      163645
Seq. ID       LIB3177-065-P1-K1-H4
Method        BLASTX
NCBI GI       g115783
BLAST score    618
E value       2.0e-64
Match length   116
% identity     100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]

```

Seq. No.	163646
Seq. ID	LIB3177-065-P1-K1-H6
Method	BLASTX
NCBI GI	g3892714
BLAST score	611
E value	1.0e-63
Match length	130
% identity	94
NCBI Description	(AL033545) trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	163647
Seq. ID	LIB3177-065-P1-K1-H7
Method	BLASTN
NCBI GI	g1769904
BLAST score	120
E value	3.0e-61
Match length	144
% identity	97
NCBI Description	A.thaliana psbP gene

Seq. No. 163648

Seq. No.	163663
Seq. ID	LIB3177-066-P1-K1-C12
Method	BLASTN
NCBI GI	g2335089
BLAST score	102
E value	3.0e-50
Match length	126
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163664
Seq. ID	LIB3177-066-P1-K1-C2
Method	BLASTN
NCBI GI	g16473
BLAST score	375
E value	0.0e+00
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

```
Seq. No.      163665
Seq. ID      LIB3177-066-P1-K1-C4
Method       BLASTX
NCBI GI      g2499535
BLAST score   352
E value      9.0e-34
Match length  82
% identity    80
NCBI Description  2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681
               (U13238) 2-oxoglutarate/malate translocator [Spinacia
               oleracea]
```

Seq. No.	163666
Seq. ID	LIB3177-066-P1-K1-C5
Method	BLASTN
NCBI GI	g2264316
BLAST score	86
E value	2.0e-40
Match length	427
% identity	39
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	163667
Seq. ID	LIB3177-066-P1-K1-C7
Method	BLASTN
NCBI GI	g3540210
BLAST score	41
E value	2.0e-14
Match length	77
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163668
Seq. ID	LIB3177-066-P1-K1-C8


```
BLAST score      348
E value         8.0e-33
Match length    71
% identity      48
NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
```

```
Seq. No.      163674
Seq. ID      LIB3177-066-P1-K1-D4
Method       BLASTX
NCBI GI      g2497733
BLAST score   203
E value      2.0e-16
Match length  53
% identity    65
NCBI Description  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
>gi_1177796 (M80567) non-specific lipid transfer protein
[Arabidopsis thaliana] >gi_3786018 (AC005499) unknown
protein [Arabidopsis thaliana]
```

Seq. No.	163675
Seq. ID	LIB3177-066-P1-K1-D5
Method	BLASTX
NCBI GI	g841208
BLAST score	309
E value	3.0e-28
Match length	128
% identity	55
NCBI Description	(U18995) trypsin inhibitor propeptide [Brassica oleracea]

Seq. No.	163676
Seq. ID	LIB3177-066-P1-K1-D7
Method	BLASTN
NCBI GI	g2642427
BLAST score	58
E value	8.0e-24
Match length	94
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163677
Seq. ID	LIB3177-066-P1-K1-D8
Method	BLASTN
NCBI GI	g17681
BLAST score	52
E value	3.0e-20
Match length	208
% identity	88
NCBI Description	A.thaliana mRNA for Wilm's tumor suppressor homologue

```
Seq. No.      163678
Seq. ID       LIB3177-066-P1-K1-D9
Method        BLASTX
NCBI GI       g4510373
BLAST score   323
E value       7.0e-30
```


BLAST score 609
E value 2.0e-63
Match length 131
% identity 92
NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No. 163689
Seq. ID LIB3177-066-P1-K1-F1
Method BLASTX
NCBI GI g4469408
BLAST score 260
E value 1.0e-22
Match length 63
% identity 81
NCBI Description (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana]

Seq. No. 163690
Seq. ID LIB3177-066-P1-K1-F10
Method BLASTX
NCBI GI g1066163
BLAST score 244
E value 1.0e-20
Match length 48
% identity 98
NCBI Description (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica napus]

Seq. No. 163691
Seq. ID LIB3177-066-P1-K1-F12
Method BLASTX
NCBI GI g731284
BLAST score 198
E value 3.0e-15
Match length 126
% identity 37
NCBI Description HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION >gi_1077482_pir_S51971 probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae) >gi_595536 (U12980) Yal048cp [Saccharomyces cerevisiae]

Seq. No. 163692
Seq. ID LIB3177-066-P1-K1-F2
Method BLASTN
NCBI GI g16470
BLAST score 171
E value 2.0e-91
Match length 187
% identity 98
NCBI Description Arabidopsis thaliana mRNA for rubisco activase

Seq. No. 163693
Seq. ID LIB3177-066-P1-K1-F3
Method BLASTX
NCBI GI g135391

>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 163703
Seq. ID LIB3177-066-P1-K1-G6
Method BLASTN
NCBI GI g1167960
BLAST score 42
E value 3.0e-14
Match length 244
% identity 30
NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds

Seq. No. 163704
Seq. ID LIB3177-066-P1-K1-G7
Method BLASTX
NCBI GI g2244798
BLAST score 324
E value 4.0e-30
Match length 62
% identity 100
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 163705
Seq. ID LIB3177-066-P1-K1-G8
Method BLASTX
NCBI GI g1769905
BLAST score 455
E value 2.0e-45
Match length 129
% identity 69
NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving complex (OEC) [Arabidopsis thaliana]

Seq. No. 163706
Seq. ID LIB3177-066-P1-K1-G9
Method BLASTX
NCBI GI g4741960
BLAST score 155
E value 1.0e-46
Match length 139
% identity 74
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 163707
Seq. ID LIB3177-066-P1-K1-H10
Method BLASTN
NCBI GI g3413696
BLAST score 297
E value 1.0e-166
Match length 305
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163708
Seq. ID	LIB3177-066-P1-K1-H2
Method	BLASTX
NCBI GI	g282865
BLAST score	323
E value	3.0e-30
Match length	71
% identity	85
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	163709
Seq. ID	LIB3177-066-P1-K1-H3
Method	BLASTX
NCBI GI	g1170373
BLAST score	668
E value	3.0e-70
Match length	130
% identity	98
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
Seq. No.	163710
Seq. ID	LIB3177-066-P1-K1-H4
Method	BLASTN
NCBI GI	g2062153
BLAST score	102
E value	3.0e-50
Match length	110
% identity	98
NCBI Description	Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163711
Seq. ID	LIB3177-066-P1-K1-H5
Method	BLASTN
NCBI GI	g4006885
BLAST score	58
E value	3.0e-24
Match length	58
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	163712
Seq. ID	LIB3177-066-P1-K1-H6
Method	BLASTN
NCBI GI	g469113
BLAST score	345
E value	0.0e+00

Match length	357
% identity	99
NCBI Description	A.thaliana (Columbia) Dr4 mRNA
Seq. No.	163713
Seq. ID	LIB3177-066-P1-K1-H7
Method	BLASTX
NCBI GI	g4510402
BLAST score	80
E value	1.2e-01
Match length	109
% identity	45
NCBI Description	(AC006587) putative AP2 domain [Arabidopsis thaliana]
Seq. No.	163714
Seq. ID	LIB3177-066-P1-K1-H8
Method	BLASTX
NCBI GI	g1702987
BLAST score	529
E value	4.0e-54
Match length	107
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]
Seq. No.	163715
Seq. ID	LIB3177-066-P1-K1-H9
Method	BLASTN
NCBI GI	g4559375
BLAST score	151
E value	2.0e-79
Match length	245
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence
Seq. No.	163716
Seq. ID	LIB3177-067-P1-K1-A10
Method	BLASTN
NCBI GI	g469113
BLAST score	393
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	A.thaliana (Columbia) Dr4 mRNA
Seq. No.	163717
Seq. ID	LIB3177-067-P1-K1-A12
Method	BLASTX
NCBI GI	g2832683
BLAST score	332
E value	6.0e-31
Match length	65
% identity	100
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 163718
 Seq. ID LIB3177-067-P1-K1-A2
 Method BLASTN
 NCBI GI g4589950
 BLAST score 210
 E value 1.0e-114
 Match length 393
 % identity 100
 NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic
 sequence, complete sequence

Seq. No. 163719
 Seq. ID LIB3177-067-P1-K1-A3
 Method BLASTN
 NCBI GI g4199934
 BLAST score 196
 E value 1.0e-106
 Match length 216
 % identity 35
 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
 complete sequence [Arabidopsis thaliana]

Seq. No. 163720
 Seq. ID LIB3177-067-P1-K1-A4
 Method BLASTX
 NCBI GI g4522012
 BLAST score 302
 E value 2.0e-27
 Match length 90
 % identity 61
 NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 163721
 Seq. ID LIB3177-067-P1-K1-A5
 Method BLASTX
 NCBI GI g886116
 BLAST score 651
 E value 2.0e-68
 Match length 125
 % identity 98
 NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
 (AF051338) xyloglucan endotransglycosylase related protein
 [Arabidopsis thaliana]

Seq. No. 163722
 Seq. ID LIB3177-067-P1-K1-A7
 Method BLASTN
 NCBI GI g16363
 BLAST score 40
 E value 3.0e-13
 Match length 103
 % identity 87
 NCBI Description A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b
 binding protein

Seq. No. 163723

Seq. ID	LIB3177-067-P1-K1-A8
Method	BLASTX
NCBI GI	g2493810
BLAST score	237
E value	4.0e-20
Match length	43
% identity	98
NCBI Description	COPROPORPHYRINOGEN III OXIDASE PRECURSOR (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) >gi_1213067_emb_CAA58038_ (X82831) coproporphyrinogen oxidase [Nicotiana tabacum]
Seq. No.	163724
Seq. ID	LIB3177-067-P1-K1-B1
Method	BLASTX
NCBI GI	g3287862
BLAST score	339
E value	5.0e-32
Match length	63
% identity	95
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >gi_2289007 (AC002335) trypsin inhibitor 2 precursor isolog [Arabidopsis thaliana]
Seq. No.	163725
Seq. ID	LIB3177-067-P1-K1-B10
Method	BLASTN
NCBI GI	g4580744
BLAST score	133
E value	4.0e-69
Match length	137
% identity	56
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence
Seq. No.	163726
Seq. ID	LIB3177-067-P1-K1-B11
Method	BLASTX
NCBI GI	g549010
BLAST score	701
E value	3.0e-74
Match length	137
% identity	100
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir_S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]
Seq. No.	163727
Seq. ID	LIB3177-067-P1-K1-B12
Method	BLASTN

Seq. No.	163732
Seq. ID	LIB3177-067-P1-K1-B8
Method	BLASTX
NCBI GI	g1778141
BLAST score	528
E value	5.0e-54
Match length	138
% identity	78
NCBI Description	(U66321) phosphate/phosphoenolpyruvate translocator precursor; PPT [Arabidopsis thaliana]

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Seq. No.      163733
Seq. ID      LIB3177-067-P1-K1-B9
Method       BLASTX
NCBI GI      g1170089
BLAST score   307
E value      1.0e-28
Match length  63
% identity    98
NCBI Description  GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                >gi_481822_pir__S39542 probable glutathione transferase (EC
                2.5.1.18) (clone ERD13) - Arabidopsis thaliana
                >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                S-transferase [Arabidopsis thaliana]
```

```
Seq. No.      163734
Seq. ID       LIB3177-067-P1-K1-C1
Method        BLASTX
NCBI GI       g4741960
BLAST score   620
E value       1.0e-64
Match length  140
% identity    85
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

```
Seq. No.      163735
Seq. ID      LIB3177-067-P1-K1-C11
Method       BLASTX
NCBI GI      g2435406
BLAST score   183
E value      7.0e-14
Match length  49
% identity    65
NCBI Description (U83490) thaumatin-like protein [Arabidopsis thaliana]
```

Seq. No.	163736
Seq. ID	LIB3177-067-P1-K1-C12
Method	BLASTN
NCBI GI	g4455348
BLAST score	140
E value	5.0e-73
Match length	263
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	163737
Seq. ID	LIB3177-067-P1-K1-C2
Method	BLASTX
NCBI GI	g3355480
BLAST score	242
E value	2.0e-20
Match length	79
% identity	56
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

```
Seq. No.      163738
Seq. ID       LIB3177-067-P1-K1-C3
Method        BLASTN
NCBI GI       g2618720
BLAST score   132
E value       3.0e-68
Match length  172
% identity    95
NCBI Description Arabidopsis thaliana early auxin-induced (IAA16) mRNA,
                  complete cds
```

```
Seq. No.      163739
Seq. ID      LIB3177-067-P1-K1-C5
Method       BLASTX
NCBI GI      g4056503
BLAST score   169
E value      3.0e-12
Match length  36
% identity    92
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      163740
Seq. ID      LIB3177-067-P1-K1-C7
Method       BLASTX
NCBI GI      g1621268
BLAST score   373
E value      5.0e-36
Match length  107
% identity    68
NCBI Description (Z81012) unknown [Ricinus communis]
```

```
Seq. No.      163741
Seq. ID      LIB3177-067-P1-K1-C8
Method       BLASTX
NCBI GI      g113026
BLAST score   614
E value      5.0e-64
Match length  132
% identity    89
NCBI Description  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
>gi_68211_pir_WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
isocitrate lyase [Brassica napus] >gi_447142 prf_1913424A
```



```
BLAST score      163
E value         8.0e-87
Match length    187
% identity      97
NCBI Description Arabidopsis thaliana gibberellin-regulated (GASA4) mRNA,
                  complete cds
```

[illegible]

Seq. No.	163754
Seq. ID	LIB3177-067-P1-K1-E5
Method	BLASTN
NCBI GI	g47594
BLAST score	85
E value	4.0e-40
Match length	161
% identity	91
NCBI Description	Synechocystis sp. ndhE gene (partial), psaC gene for photosystem I iron-sulfur protein and ndhD-like ORF

```
Seq. No.      163755
Seq. ID      LIB3177-067-P1-K1-E6
Method       BLASTN
NCBI GI      g3283056
BLAST score   48
E value      3.0e-18
Match length  127
% identity    84
NCBI Description Arabidopsis thaliana one helix protein (OHP) mRNA, complete cds
```

```
Seq. No.      163756
Seq. ID      LIB3177-067-P1-K1-E7
Method       BLASTX
NCBI GI      g132110
BLAST score   393
E value      2.0e-38
Match length  79
% identity    96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
```

(X14564) ribulose biphosphate carboxylase [Arabidopsis thaliana]

```
Seq. No.      163757
Seq. ID      LIB3177-067-P1-K1-E8
Method       BLASTX
NCBI GI      g115783
BLAST score   601
E value      1.0e-62
Match length  114
% identity    99
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

Seq. No.	163758
Seq. ID	LIB3177-067-P1-K1-E9
Method	BLASTN
NCBI GI	g343376
BLAST score	32
E value	9.0e-09
Match length	59
% identity	90
NCBI Description	Spinach rps4 gene encoding ribosomal protein S4, complete cds, with Thr-tRNA and Ser-tRNA genes

```
Seq. No.      163759
Seq. ID      LIB3177-067-P1-K1-F1
Method       BLASTX
NCBI GI      g1170089
BLAST score   260
E value      3.0e-23
Match length  64
% identity   86
NCBI Description  GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                >gi_481822_pir__S39542 probable glutathione transferase (EC
                2.5.1.18) (clone ERD13) - Arabidopsis thaliana
                >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                S-transferase [Arabidopsis thaliana]
```

```
Seq. No.      163760
Seq. ID       LIB3177-067-P1-K1-F11
Method        BLASTX
NCBI GI       g4454470
BLAST score   344
E value       1.0e-32
Match length  109
% identity    68
NCBI Description (AC006234) putative sugar transporter [Arabidopsis
thaliana]
```

```
Seq. No.      163761
Seq. ID      LIB3177-067-P1-K1-F12
Method       BLASTX
NCBI GI      q2499327
```



```
>gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of  
mitochondrial F1-ATPase [Arabidopsis thaliana]
```

```
Seq. No.      163766
Seq. ID      LIB3177-067-P1-K1-G11
Method       BLASTX
NCBI GI      g4538903
BLAST score   139
E value      9.0e-09
Match length  72
% identity    43
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      163767
Seq. ID      LIB3177-067-P1-K1-G12
Method       BLASTX
NCBI GI      g3695383
BLAST score   250
E value      1.0e-21
Match length  61
% identity    82
NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:
PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
thaliana]
```

Seq. No.	163768
Seq. ID	LIB3177-067-P1-K1-G2
Method	BLASTX
NCBI GI	g2911042
BLAST score	357
E value	2.0e-34
Match length	72
% identity	100
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	163769
Seq. ID	LIB3177-067-P1-K1-G3
Method	BLASTX
NCBI GI	g4490732
BLAST score	567
E value	1.0e-58
Match length	120
% identity	88
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

```
Seq. No.      163770
Seq. ID      LIB3177-067-P1-K1-G4
Method       BLASTX
NCBI GI      g2815905
BLAST score   290
E value      4.0e-26
Match length  98
% identity    58
NCBI Description (AF043734) Pros45 proteosome subunit homolog [Drosophila
melanogaster]
```



```

BLAST score      624
E value         2.0e-66
Match length    132
% identity      98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603_pir_A29280 chlorophyll
                  a/b-binding protein abl65 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_(X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_(X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]

```

```
Seq. No.      163776
Seq. ID       LIB3177-067-P1-K1-H11
Method        BLASTX
NCBI GI       g1732570
BLAST score   277
E value       3.0e-25
Match length  73
% identity    77
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
```

```
Seq. No.      163777
Seq. ID      LIB3177-067-P1-K1-H12
Method       BLASTX
NCBI GI      g115385
BLAST score   687
E value      1.0e-72
Match length  131
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
```

```
Seq. No.      163778
Seq. ID       LIB3177-067-P1-K1-H2
Method        BLASTN
NCBI GI       g3212846
BLAST score    200
E value        1.0e-109
Match length   244
% identity     100
NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic
sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.      163779
Seq. ID      LIB3177-067-P1-K1-H3
Method       BLASTN
NCBI GI      g4056476
BLAST score   113
E value      7.0e-57
Match length  194
% identity    95
NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic
sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 163780

BLAST score 561
 E value 8.0e-58
 Match length 109
 % identity 98
 NCBI Description (AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No. 163785
 Seq. ID LIB3177-068-P1-K1-A11
 Method BLASTX
 NCBI GI g118514
 BLAST score 179
 E value 2.0e-25
 Match length 88
 % identity 65
 NCBI Description TURGOR-RESPONSIVE PROTEIN 26G >gi_100051_pir_S11863 aldehyde dehydrogenase homolog - garden pea >gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum sativum]

Seq. No. 163786
 Seq. ID LIB3177-068-P1-K1-A12
 Method BLASTN
 NCBI GI g3421079
 BLAST score 353
 E value 0.0e+00
 Match length 357
 % identity 100
 NCBI Description Arabidopsis thaliana 20S proteasome subunit PAD1 (PAD1) mRNA, complete cds

Seq. No. 163787
 Seq. ID LIB3177-068-P1-K1-A2
 Method BLASTX
 NCBI GI g132110
 BLAST score 582
 E value 2.0e-60
 Match length 116
 % identity 96
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 163788
 Seq. ID LIB3177-068-P1-K1-A3
 Method BLASTN
 NCBI GI g2244829
 BLAST score 228
 E value 1.0e-125
 Match length 404
 % identity 98


```
Seq. No.          163794
Seq. ID           LIB3177-068-P1-K1-B10
Method            BLASTX
NCBI GI           g131398
BLAST score       554
E value           5.0e-57
Match length      140
% identity        81
NCBI Description  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi_72714_pir_F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                  come from this gene. [Arabidopsis
```

```
Seq. No.      163795
Seq. ID      LIB3177-068-P1-K1-B11
Method       BLASTX
NCBI GI      g2062161
BLAST score   588
E value      4.0e-61
Match length  128
% identity    53
NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
```

Seq. No.	163796
Seq. ID	LIB3177-068-P1-K1-B12
Method	BLASTN
NCBI GI	g438448
BLAST score	34
E value	4.0e-10
Match length	38
% identity	97
NCBI Description	Arabidopsis thaliana carbonic anhydrase (ca180) mRNA, complete cds

Seq. No.	163797
Seq. ID	LIB3177-068-P1-K1-B2
Method	BLASTX
NCBI GI	g4741940
BLAST score	536
E value	6.0e-55
Match length	118
% identity	60
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

```
Seq. No.      163798
Seq. ID      LIB3177-068-P1-K1-B3
Method       BLASTN
NCBI GI      g2760169
BLAST score   186
E value      1.0e-100
```



```
Seq. ID      LIB3177-068-P1-K1-D2
Method       BLASTX
NCBI GI      g132074
BLAST score   517
E value      7.0e-53
Match length  105
% identity    95
NCBI Description  RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir_RKMUA1
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                A1 precursor - Arabidopsis thaliana
```

Seq. No.	163819
Seq. ID	LIB3177-068-P1-K1-D3
Method	BLASTN
NCBI GI	g2459406
BLAST score	202
E value	1.0e-110
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163820
Seq. ID      LIB3177-068-P1-K1-D4
Method       BLASTN
NCBI GI      g4519194
BLAST score   257
E value      1.0e-142
Match length 288
% identity    97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                MHM17, complete sequence
```

```
Seq. No.      163821
Seq. ID      LIB3177-068-P1-K1-D5
Method       BLASTX
NCBI GI      g1370186
BLAST score   516
E value      2.0e-52
Match length  101
% identity    98
NCBI Description (Z73942) RAB7C [Lotus japonicus]
```

```
Seq. No.      163822
Seq. ID      LIB3177-068-F1-K1-D6
Method       BLASTX
NCBI GI      g4582787
BLAST score   334
E value      2.0e-31
Match length  77
% identity    83
NCBI Description (AJ012281) adenosine kinase [Zea mays]
```

```
Seq. No.      163823
Seq. ID      LIB3177-068-P1-K1-D7
Method       BLASTX
```



```
Seq. No.      163828
Seq. ID      LIB3177-068-P1-K1-E11
Method       BLASTX
NCBI GI      g115783
BLAST score   698
E value      6.0e-74
Match length  136
% identity    97
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

Seq. No.	163829
Seq. ID	LIB3177-068-P1-K1-E12
Method	BLASTX
NCBI GI	g3286693
BLAST score	618
E value	2.0e-64
Match length	128
% identity	98
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	163830
Seq. ID	LIB3177-068-P1-K1-E2
Method	BLASTX
NCBI GI	g1169601
BLAST score	743
E value	4.0e-79
Match length	146
% identity	99
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_493068 (U09503) chloroplast omega-6 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	163831
Seq. ID	LIB3177-068-P1-K1-E3
Method	BLASTN
NCBI GI	g4581084
BLAST score	280
E value	1.0e-156
Match length	332
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

```
Seq. No.          163832
Seq. ID          LIB3177-068-P1-K1-E4
Method           BLASTN
NCBI GI          g4713943
BLAST score      98
E value          3.0e-48
Match length     146
% identity       92
NCBI Description  Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
                  complete sequence
```

```
Seq. No.      163833
Seq. ID      LIB3177-068-P1-K1-E5
Method       BLASTX
NCBI GI      g4586256
BLAST score   247
E value      4.0e-21
Match length  62
% identity    81
NCBI Description (AL049640) probable photosystem I chain XI precursor
               [Arabidopsis thaliana]
```

Seq. No.	163834
Seq. ID	LIB3177-068-P1-K1-E6
Method	BLASTN
NCBI GI	g3869069
BLAST score	56
E value	1.0e-22
Match length	389
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163835
Seq. ID      LIB3177-068-P1-K1-E7
Method       BLASTX
NCBI GI      g115783
BLAST score   508
E value      9.0e-52
Match length  95
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

```
Seq. No.      163836
Seq. ID      LIB3177-068-P1-K1-F1
Method       BLASTX
NCBI GI      g421826
BLAST score   618
E value      2.0e-64
Match length  141
% identity    82
NCBI Description  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                thaliana]
```

```
Seq. No.      163837
Seq. ID      LIB3177-068-P1-K1-F10
Method       BLASTX
NCBI GI      g4741960
BLAST score   478
E value      4.0e-48
Match length  111
% identity    82
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

```
Seq. No.      163838
Seq. ID      LIB3177-068-P1-K1-F11
Method       BLASTN
NCBI GI      g4519190
BLAST score   136
E value      2.0e-70
Match length  464
% identity    98
NCBI Description  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
K6A12, complete sequence
```

```
Seq. No.      163839
Seq. ID      LIB3177-068-P1-K1-F2
Method       BLASTX
NCBI GI      g3914442
BLAST score   518
E value      9.0e-53
Match length  140
% identity    74
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
```

Seq. No.	163840
Seq. ID	LIB3177-068-P1-K1-F3
Method	BLASTX
NCBI GI	g1145697
BLAST score	514
E value	2.0e-52
Match length	106
% identity	53
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	163841
Seq. ID	LIB3177-068-P1-K1-F4
Method	BLASTN
NCBI GI	g4206762
BLAST score	49
E value	2.0e-18
Match length	334
% identity	40
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLPL) mRNA, complete cds

Seq. No.	163842
Seq. ID	LIB3177-068-P1-K1-F5
Method	BLASTN
NCBI GI	g3299824
BLAST score	427
E value	0.0e+00
Match length	471
% identity	97
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]


```
Seq. No.      163848
Seq. ID      LIB3177-068-P1-K1-G12
Method       BLASTX
NCBI GI      g4539009
BLAST score   661
E value      2.0e-69
Match length  156
% identity    76
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      163849
Seq. ID      LIB3177-068-P1-K1-G2
Method       BLASTX
NCBI GI      g1175010
BLAST score   317
E value      1.0e-46
Match length  113
% identity    88
NCBI Description  PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082
                plasma membrane intrinsic protein 1a - Arabidopsis thaliana
                >gi_472873_emb_CAA53475_(X75881) plasma membrane intrinsic
                protein 1a [Arabidopsis thaliana]
```

[illegible]

```
Seq. No.          163851
Seq. ID           LIB3177-068-P1-K1-G5
Method            BLASTN
NCBI GI           g4589412
BLAST score       46
E value           1.0e-16
Match length      155
% identity        86
NCBI Description   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F6N7, complete sequence
```

Seq. No.	163852
Seq. ID	LIB3177-068-P1-K1-G6
Method	BLASTX
NCBI GI	g3914442
BLAST score	424
E value	7.0e-42

Variable	Mean	SD	Min	Max
Age	35.5	10.5	20	55
Gender	Male	Female		
Marital Status	Married	Single		
Education	High School	College		
Occupation	Manager	Worker		
Income	\$30,000	\$40,000		
Health Status	Good	Fair		
Exercise Frequency	Weekly	Monthly		
Stress Level	Low	High		
Sleep Quality	Good	Poor		
Dietary Habits	Healthy	Unhealthy		
Alcohol Consumption	Occasional	Frequent		
Tobacco Use	Non-user	User		
Family Size	2	3		
Home Ownership	Owner	Renter		
Commute Time	30 min	45 min		
Work Hours	40 hrs/week	50 hrs/week		
Job Satisfaction	High	Low		
Life Satisfaction	High	Low		
Overall Well-being	Good	Fair		

Seq. No.	163863
Seq. ID	LIB3177-068-P1-K1-H6
Method	BLASTX
NCBI GI	g3449041
BLAST score	486
E value	3.0e-49
Match length	90
% identity	97
NCBI Description	(U73462) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	163864
Seq. ID	LIB3177-068-P1-K1-H7
Method	BLASTN
NCBI GI	g4159706
BLAST score	104
E value	7.0e-52
Match length	127
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

```
Seq. No.      163865
Seq. ID      LIB3177-068-P1-K1-H8
Method       BLASTX
NCBI GI      g166835
BLAST score   525
E value      7.0e-54
Match length  100
% identity    100
NCBI Description (M86720) ribulose biphosphate carboxylase/oxygenase
activase [Arabidopsis thaliana] >gi_2642170 (AC003000)
Rubisco activase [Arabidopsis thaliana]
```

Seq. No.	163866
Seq. ID	LIB3177-068-P1-K1-H9
Method	BLASTN
NCBI GI	g600388
BLAST score	285
E value	1.0e-159
Match length	306
% identity	98
NCBI Description	A.thaliana UbcAT3 mRNA for ubiquitin conjugating enzyme E2

```
Seq. No.          163867
Seq. ID           LIB3177-069-P1-K1-A10
Method            BLASTN
NCBI GI           g4519192
BLAST score       258
E value           1.0e-143
Match length      262
% identity        100
NCBI Description   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
```

Seq. No.	163868
Seq. ID	LIB3177-069-P1-K1-A11

Seq. No.	163883
Seq. ID	LIB3177-069-P1-K1-B7
Method	BLASTX
NCBI GI	g4263525
BLAST score	602
E value	1.0e-62
Match length	141
% identity	85
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	163884
Seq. ID	LIB3177-069-P1-K1-C11
Method	BLASTX
NCBI GI	g2052379
BLAST score	571
E value	4.0e-59
Match length	106
% identity	99
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No.	163885
Seq. ID	LIB3177-069-P1-K1-C12
Method	BLASTX
NCBI GI	g1653089
BLAST score	243
E value	1.0e-20
Match length	80
% identity	56
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	163886
Seq. ID	LIB3177-069-P1-K1-C2
Method	BLASTX
NCBI GI	g4406816
BLAST score	545
E value	9.0e-59
Match length	119
% identity	97
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	163887
Seq. ID	LIB3177-069-P1-K1-C3
Method	BLASTX
NCBI GI	g132110
BLAST score	670
E value	1.0e-70
Match length	125
% identity	98
NCBI Description	RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphtosphate carboxylase [Arabidopsis thaliana]

Seq. No. 163888


```

Match length      95
% identity        89
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]

```

```
Seq. No.          163923
Seq. ID          LIB3177-069-P1-K1-H11
Method           BLASTX
NCBI GI          g3914117
BLAST score      582
E value          3.0e-60
Match length     144
% identity       81
NCBI Description  NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP
                  KINASE II) >gi_3093480 (AF017640) nucleoside diphosphate
                  kinase type 2 [Arabidopsis thaliana]
```

Seq. No.	163924
Seq. ID	LIB3177-069-P1-K1-H12
Method	BLASTX
NCBI GI	g4566505
BLAST score	262
E value	4.0e-23
Match length	84
% identity	60
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

```
Seq. No.      163925
Seq. ID      LIB3177-069-P1-K1-H2
Method       BLASTX
NCBI GI      g3080401
BLAST score   587
E value      7.0e-61
Match length  116
% identity    100
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
               >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
               [Arabidopsis thaliana]
```

Seq. No.	163926
Seq. ID	LIB3177-069-P1-K1-H3
Method	BLASTN
NCBI GI	g3402745
BLAST score	166
E value	3.0e-88
Match length	268
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	163927
Seq. ID	LIB3177-069-P1-K1-H4
Method	BLASTN
NCBI GI	q4519185

Seq. No.	163994
Seq. ID	LIB3177-070-P1-K1-G2
Method	BLASTN
NCBI GI	g4756963
BLAST score	231
E value	1.0e-127
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

```
Seq. No.      163995
Seq. ID      LIB3177-070-P1-K1-G3
Method       BLASTX
NCBI GI      g1351271
BLAST score   185
E value      9.0e-14
Match length  41
% identity    90
NCBI Description  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir__S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme
[Spinacia oleracea]
```

```
Seq. No.      163996
Seq. ID      LIB3177-070-P1-K1-G4
Method       BLASTX
NCBI GI      g4741960
BLAST score   500
E value      1.0e-50
Match length  116
% identity    84
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

Seq. No.	163997
Seq. ID	LIB3177-070-P1-K1-G5
Method	BLASTN
NCBI GI	g4567237
BLAST score	404
E value	0.0e+00
Match length	478
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

```
Seq. No.      163998
Seq. ID      LIB3177-070-P1-K1-G6
Method       BLASTN
NCBI GI      g2749918
BLAST score   215
E value      1.0e-117
Match length  295
% identity    98
NCBI Description Arabidopsis thaliana chromosome I BAC F3I6 genomic
sequence, complete sequence [Arabidopsis thaliana]
```


